



SEQUENCE LISTING

<110> Smith, Michael D.
Potter, Robert J.
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<120> Thermostable Reverse Transcriptases and Uses Thereof

<130> 0942.5040001/RWE/MTT

<140> US 09/845,157

<141> 2001-05-01

<150> US 60/207,196

<151> 2000-05-26

<160> 8

<170> PatentIn version 3.0

<210> 1

<211> 2151

<212> DNA

<213> Moloney-Murine Leukemia Virus

<220>

<221> CDS

<222> (1)..(2151)

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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys His			
20	25	30	
atg acc cta aat ata gaa gat gag tat cgg cta cat gag acc tca aaa			144
Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys			
35	40	45	
gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag			192
Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln			
50	55	60	
gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct			240
Ala Trp Ala Glu Thr Gly Met Gly Leu Ala Val Arg Gln Ala Pro			
65	70	75	80
ctg atc ata ctt ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa			288
Leu Ile Ile Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln			
85	90	95	
tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag			336
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln			
100	105	110	
aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac			384
Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn			
115	120	125	
acg ccc ctg cta ccc gtc aag aaa ccc ggg act aat gat tac agg cct			432
Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro			
130	135	140	
gtc caa gat ctg aga gag gtc aac aaa cgc gta gaa gac atc cac ccc			480
Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro			
145	150	155	160
acc gta ccc aac ccc tac aac ctc ttg agt ggg ctc cca ccg tcc cac			528
Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His			
165	170	175	
cag tgg tac act gtt cta gac tta aaa gat gcc ttt ttc tgc ctg aga			576
Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg			
180	185	190	
ctc cac ccg acg tct cag cct ctc ttc gcc ttt gaa tgg aga gac cca			624
Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro			
195	200	205	
gag atg gga atc tct ggc caa cta acc tgg acc aga ctc cca cag gga			672
Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly			
210	215	220	
ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg cgc aga gac cta			720
Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu			

225	230	235	240	
gca gac ttc cgg atc cag cac cca gac ttg atc ctg cta cag tac gta Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val 245	250	255		768
gat gac tta ctg ctg gcc act tct gag ctc gac tgc caa caa ggt Asp Asp Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly 260	265	270		816
act cg ^g gcc ctg tta caa acc cta gga gac ctc ggg tat cg ^g gcc tcg Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser 275	280	285		864
gcc aag aaa gcc caa att tgc cag aaa cag gtc aag tat ctg ggg tat Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr 290	295	300		912
ctt cta aaa gag ggt cag aga tgg ctg act gag gcc aga aaa gag act Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr 305	310	315	320	960
gtg atg ggg cag cct act ccg aag acc ccg cg ^g caa cta agg gag ttc Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe 325	330	335		1008
cta ggg acg gca ggc ttc tgt cgc ctc tgg atc cct ggg ttt gca gaa Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu 340	345	350		1056
atg gca gcc ccc ttg tac cct ctc acc aaa acg ggg act ctg ttt aat Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn 355	360	365		1104
tgg ggc cca gac caa caa aag gcc tat caa gaa atc aag caa gct ctt Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu 370	375	380		1152
cta act gcc cca gcc ctg ggg ttg cca gat ttg act aag ccc ttt gaa Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu 385	390	395	400	1200
ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt gtc cta acg caa Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln 405	410	415		1248
aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg tcc aaa aag cta Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu 420	425	430		1296
gac cca gta gca gct ggg tgg ccc cct tgc cta ccg atg gta gca gcc Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala 435	440	445		1344
att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro 450	455	460		1392

cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro 465 470 475 480	1440
ccc gat cga tgg ctt tcc aac gcc cg ^g atg act cac tat cag gcc ttg Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu 485 490 495	1488
ctt ttg gac acg gac cg ^g gtc cag ttc gga ccg gtg gta gcc ctg aac Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn 500 505 510	1536
ccg gct aca ctg ctc cca ctg cct gag gaa ggg ctg cag cac aac tgc Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys 515 520 525	1584
ctt gat atc ctg gcc gaa gcc cac gga acc cga ccc gac cta acg gac Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp 530 535 540	1632
cag ccg ctc cca gac gcc gac cac acc tgg tac acg ggt gga tcc agt Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser 545 550 555 560	1680
ctc ttg caa gag gga cag cgt aag gc ^g gga gct gc ^g gtg acc acc gag Leu Leu Gln Glu Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu 565 570 575	1728
acc gag gta atc tgg gct aaa gcc ctg cca gcc ggg aca tcc gct cag Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln 580 585 590	1776
cg ^g gct cag ctg ata gca ctc acc cag gcc cta agg atg gca gaa ggt Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly 595 600 605	1824
aag aag cta aat gtt tat acg aat tcc cgt tat gct ttt gct act gcc Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala 610 615 620	1872
cat atc cat gga gaa ata tac aga agg cgt ggg ttg ctc aca tca gaa His Ile His Gly Glu Ile Tyr Arg Arg Gly Leu Leu Thr Ser Glu 625 630 635 640	1920
ggc aaa gag atc aaa aat aag gac gag ata ttg gcc cta cta aaa gcc Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala 645 650 655	1968
ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt cca gga cat caa Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln 660 665 670	2016
aag gga cac agc gcc gag gct aga ggc aac cg ^g atg gct gac caa gcg Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala 675 680 685	2064

gcc cga aag gca gcc atc aca gag aat cca gac acc tct acc ctc ctc 2112
Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu
690 695 700

ata gaa aat tca tca ccc aat tcc cgc tta att aat taa 2151
Ile Glu Asn Ser Ser Pro Asn Ser Arg Leu Ile Asn
705 710 715

<210> 2

<211> 716

<212> PRT

<213> Moloney-Murine Leukemia Virus

<400> 2

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Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
35 40 45

Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
50 55 60

Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
65 70 75 80

Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
85 90 95

Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
100 105 110

Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
115 120 125

Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
130 135 140

Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro

145

150

155

160

Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
165 170 175

Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
180 185 190

Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
195 200 205

Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
210 215 220

Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu
225 230 235 240

Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
245 250 255

Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
260 265 270

Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser
275 280 285

Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
290 295 300

Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
305 310 315 320

Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
325 330 335

Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu
340 345 350

Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
355 360 365

Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
370 375 380

Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu
385 390 395 400

Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
405 410 415

Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
420 425 430

Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
435 440 445

Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
450 455 460

Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
465 470 475 480

Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
485 490 495

Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
500 505 510

Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
515 520 525

Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp
530 535 540

Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser
545 550 555 560

Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu
565 570 575

Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln
580 585 590

Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly
595 600 605

Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala
610 615 620

His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu
625 630 635 640

Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala
645 650 655

Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln
660 665 670

Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
675 680 685

Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu
690 695 700

Ile Glu Asn Ser Ser Pro Asn Ser Arg Leu Ile Asn
705 710 715

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<211> 47

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<213> Artificial

<220>

<223> Oligonucleotide template

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<211> 18

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide primer

<400> 4
cttccattca cacactgc

18

<210> 5

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide primer

<400> 5
gaagatcgca ctccagccag c

21

<210> 6

<211> 298

<212> DNA

<213> Escherichia coli

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gctatgacca tgattacgcc aagcttgcatt gcctgcaggc cgactctaga ggatccccgg 180
gtaccgagct cgaatttcaact ggccgtcggtt ttacaacgtc gtgactggaa aaaccctggc 240
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<212> DNA

<213> Moloney-Murine Leukemia Virus

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<221> CDS

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Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
20 25 30
gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct 144
Ala Trp Ala Glu Thr Gly Met Gly Leu Ala Val Arg Gln Ala Pro
35 40 45
ctg atc ata cct ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa 192
Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
50 55 60
tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag 240
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
65 70 75 80
aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac 288
Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
85 90 95
acg ccc ctg cta ccc gtt aag aaa cca ggg act aat gat tat agg cct 336
Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
100 105 110
gtc cag gat ctg aga gaa gtc aac aag cgg gtg gaa gac atc cac ccc 384
Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
115 120 125
acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc aag cgg gtg gaa 432
Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Lys Arg Val Glu
130 135 140
gac atc cac ccc acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc 480
Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu
145 150 155 160
cca ccg tcc cac cag tgg tac act gtg ctt gat tta aag gat gcc ttt 528
Pro Pro Ser His Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe
165 170 175
ttc tgc ctg aga ctc cac ccc acc agt cag cct ctc ttc gcc ttt gag 576
Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu
180 185 190

tgg aga gat cca gag atg gga atc tca gga caa ttg acc tgg acc aga	624
Trp Arg Asp Pro Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg	
195 200 205	
ctc cca cag ggt ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg	672
Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu	
210 215 220	
cac aga gac cta gca gac ttc cgg atc cag cac cca gac ttg atc ctg	720
His Arg Asp Leu Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu	
225 230 235 240	
cta cag tac gtg gat gac tta ctg ctg gcc gcc act tct gag cta gac	768
Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp	
245 250 255	
tgc caa caa ggt act cgg gcc ctg tta caa acc cta ggg aac ctc ggg	816
Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly	
260 265 270	
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Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys	
275 280 285	
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Tyr Leu Gly Tyr Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala	
290 295 300	
aga aaa gag act gtg atg ggg cag cct act ccg aag acc cct cga caa	960
Arg Lys Glu Thr Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln	
305 310 315 320	
cta agg gag ttc cta ggg acg gca ggc ttc tgt cgc ctc tgg atc cct	1008
Leu Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro	
325 330 335	
ggg ttt gca gaa atg gca gcc ccc ttg tac cct ctc acc aaa acg ggg	1056
Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly	
340 345 350	
act ctg ttt aat tgg ggc cca gac caa caa aag gcc tat caa gaa atc	1104
Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile	
355 360 365	
aag caa gct ctt cta act gcc cca gcc ctg ggg ttg cca gat ttg act	1152
Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr	
370 375 380	
aag ccc ttt gaa ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt	1200
Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly	
385 390 395 400	
gtc cta acg caa aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg	1248
Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu	
405 410 415	
tcc aaa aag cta gac cca gta gca gct ggg tgg ccc cct tgc cta cgg	1296

Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg			
420	425	430	
atg gta gca gcc att gcc gta ctg aca aag gat gca ggc aag cta acc			1344
Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr			
435	440	445	
atg gga cag cca cta gtc att ctg gcc ccc cat gca gta gag gca cta			1392
Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu			
450	455	460	
gtc aaa caa ccc ccc gac cgc tgg ctt tcc aac gcc cgg atg act cac			1440
Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His			
465	470	475	480
tat cag gcc ttg ctt ttg gac acg gac cgg gtc cag ttc gga ccc gtg			1488
Tyr Gln Ala Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val			
485	490	495	
gta gcc ctg aac ccg gct acg ctg ctc cca ctg cct gag gaa ggg ctg			1536
Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu			
500	505	510	
caa cac aac tgc ctt gat aat tcc cgc tta att aat taa			1575
Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn			
515	520		
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<212> PRT			
<213> Moloney-Murine Leukemia Virus			
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Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln			
20	25	30	
Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro			
35	40	45	
Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln			
50	55	60	
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln			

65

70

75

80

Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
85 90 95

Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
100 105 110

Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
115 120 125

Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Lys Arg Val Glu
130 135 140

Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu
145 150 155 160

Pro Pro Ser His Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe
165 170 175

Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu
180 185 190

Trp Arg Asp Pro Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg
195 200 205

Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu
210 215 220

His Arg Asp Leu Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu
225 230 235 240

Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp
245 250 255

Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly
260 265 270

Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys
275 280 285

Tyr Leu Gly Tyr Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala
290 295 300

Arg Lys Glu Thr Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln
305 310 315 320

Leu Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro
325 330 335

Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly
340 345 350

Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile
355 360 365

Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr
370 375 380

Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly
385 390 395 400

Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu
405 410 415

Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg
420 425 430

Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr
435 440 445

Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu
450 455 460

Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His
465 470 475 480

Tyr Gln Ala Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val
485 490 495

Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu
500 505 510

Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn
515 520



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Michael D. SMITH *et al.*

Appl. No.: 09/845,157

Filed: May 1, 2001

For: **Thermostable Reverse Transcriptases
and Uses Thereof**

Confirmation No.: 2674

Art Unit: 1637

Examiner: Fredman, Jeffrey N.

Atty. Docket: 0942.5040001/RWE/HCC

**Amendment and Submission of Substitute Sequence Listing
Under 37 C.F.R. § 1.825(a)**

Commissioner for Patents
PO Box 1450
Alexandria, VA 22313-1450

Sir:

In compliance with 37 C.F.R. § 1.825(a), Applicants submit substitute sheets to amend the paper copy of the Sequence Listing.

In the Specification:

Please cancel the existing Sequence Listing for the above-identified application, replace it with the substitute Sequence Listing appended hereto, and insert the same at the end of the application.

Remarks

The changes made in the sequence listing do not include new matter. Support for these amendments can be found in the specification as originally filed on page 34, paragraph 0092, wherein U.S. Patent No. 5,668,005 is incorporated by reference. The specification has been amended to direct the entry of this corrected Sequence Listing at the end of the above identified application.

In accordance with 37 C.F.R. § 1.825(a), this submission contains no new matter.

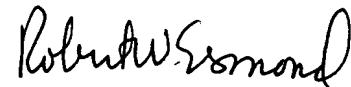
In accordance with 37 C.F.R. § 1.825(b), the paper copy of the Sequence Listing and the computer readable copy of the Sequence Listing submitted herewith are the same.

Summary

It is respectfully believed this application is now in condition for allowance. Early notice to this effect is earnestly solicited.

Respectfully submitted,

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